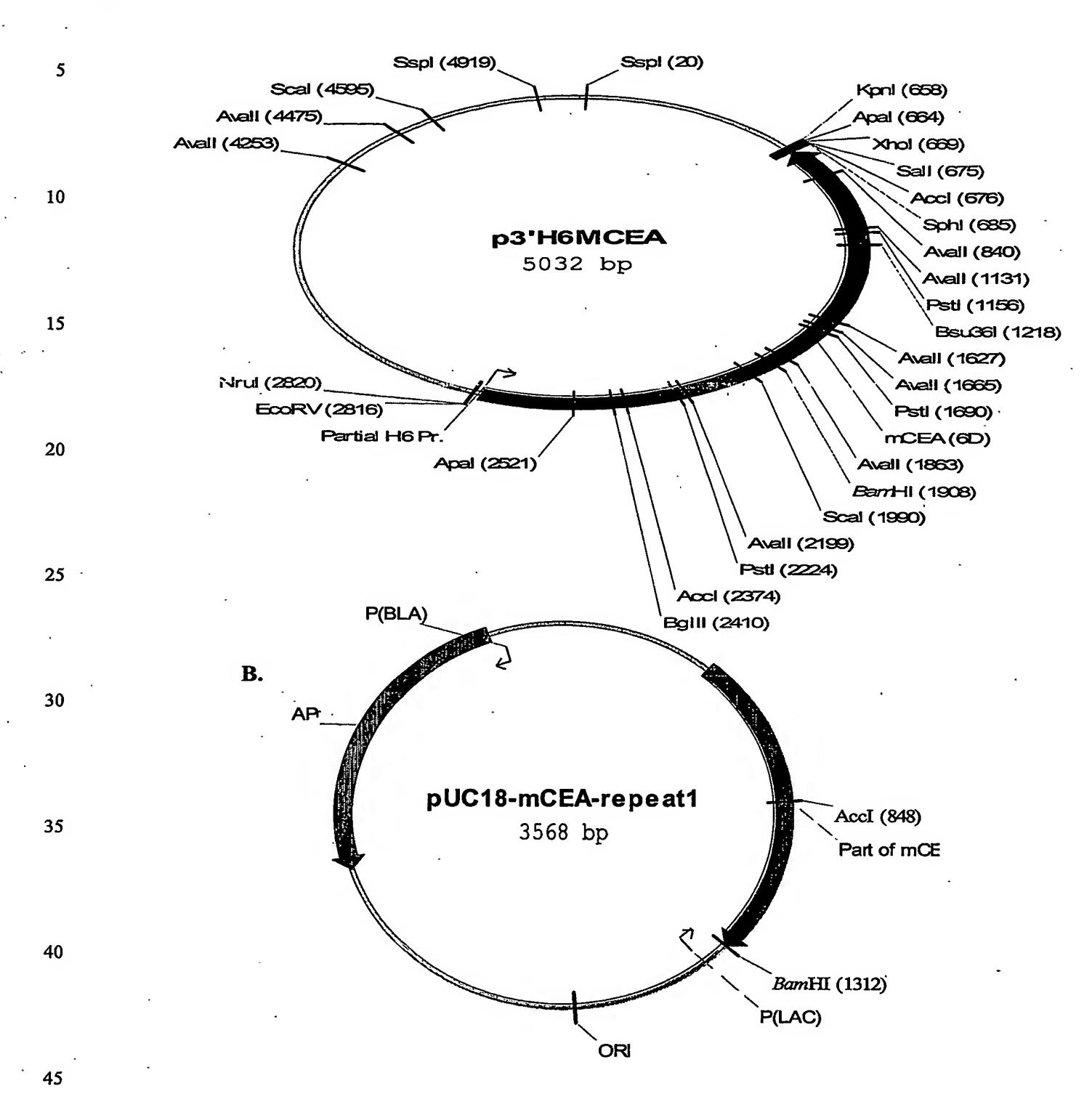
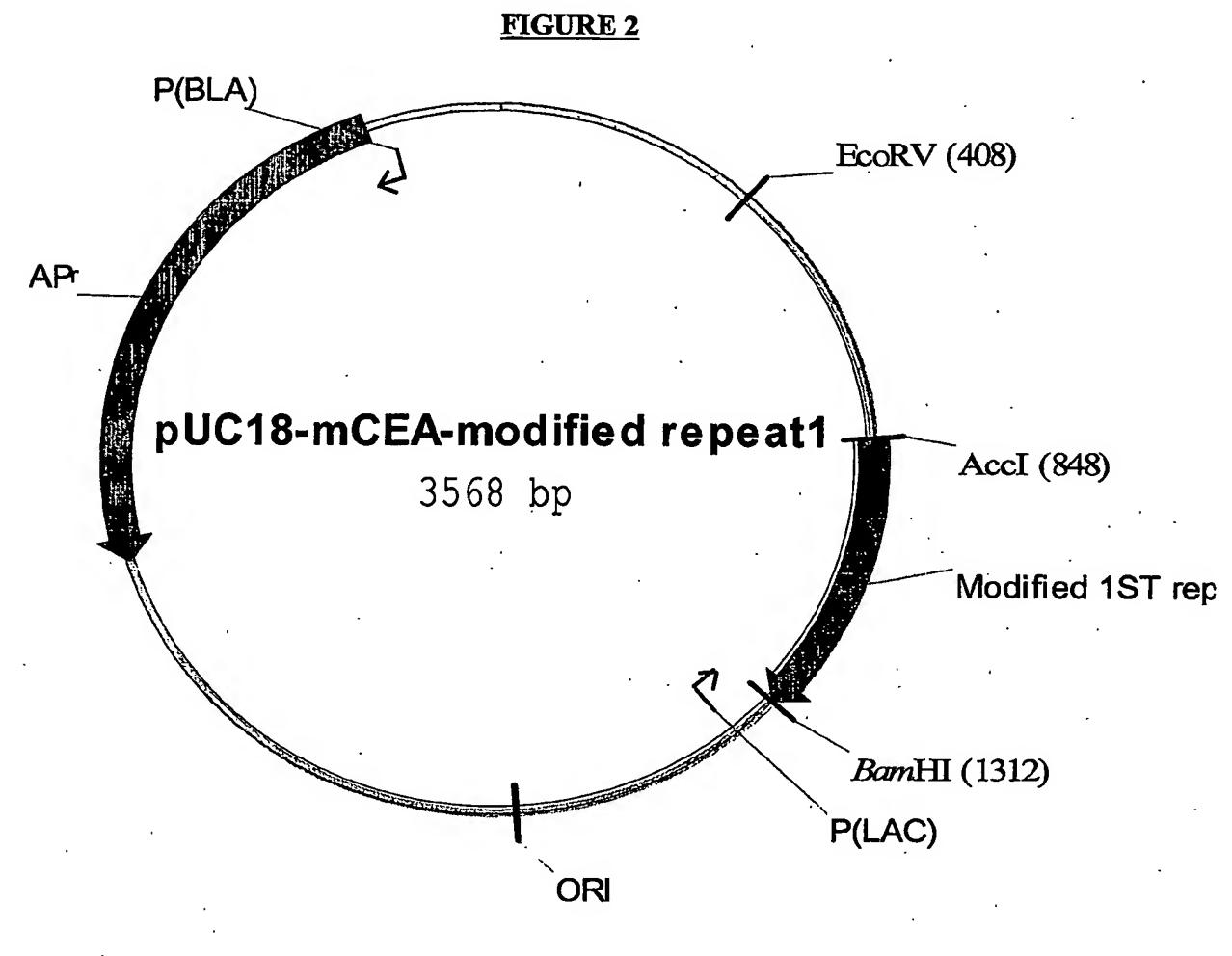
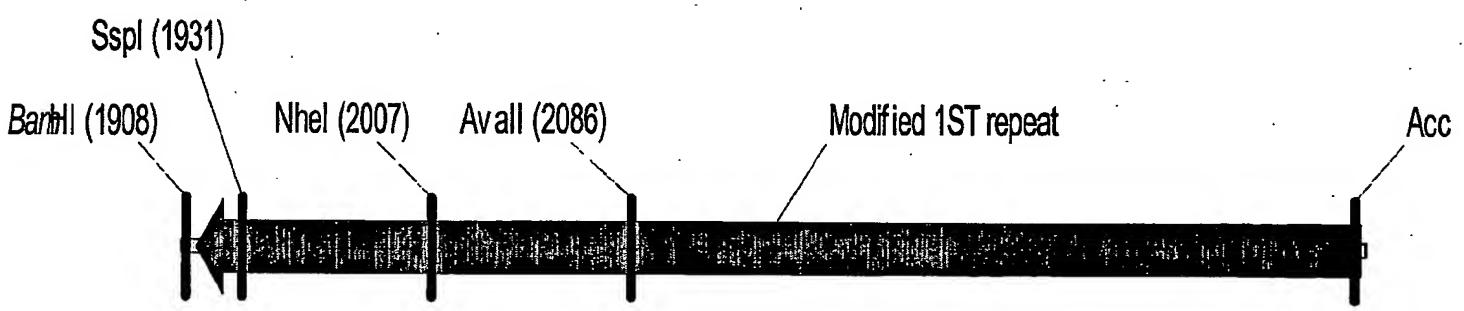
FIGURE 1

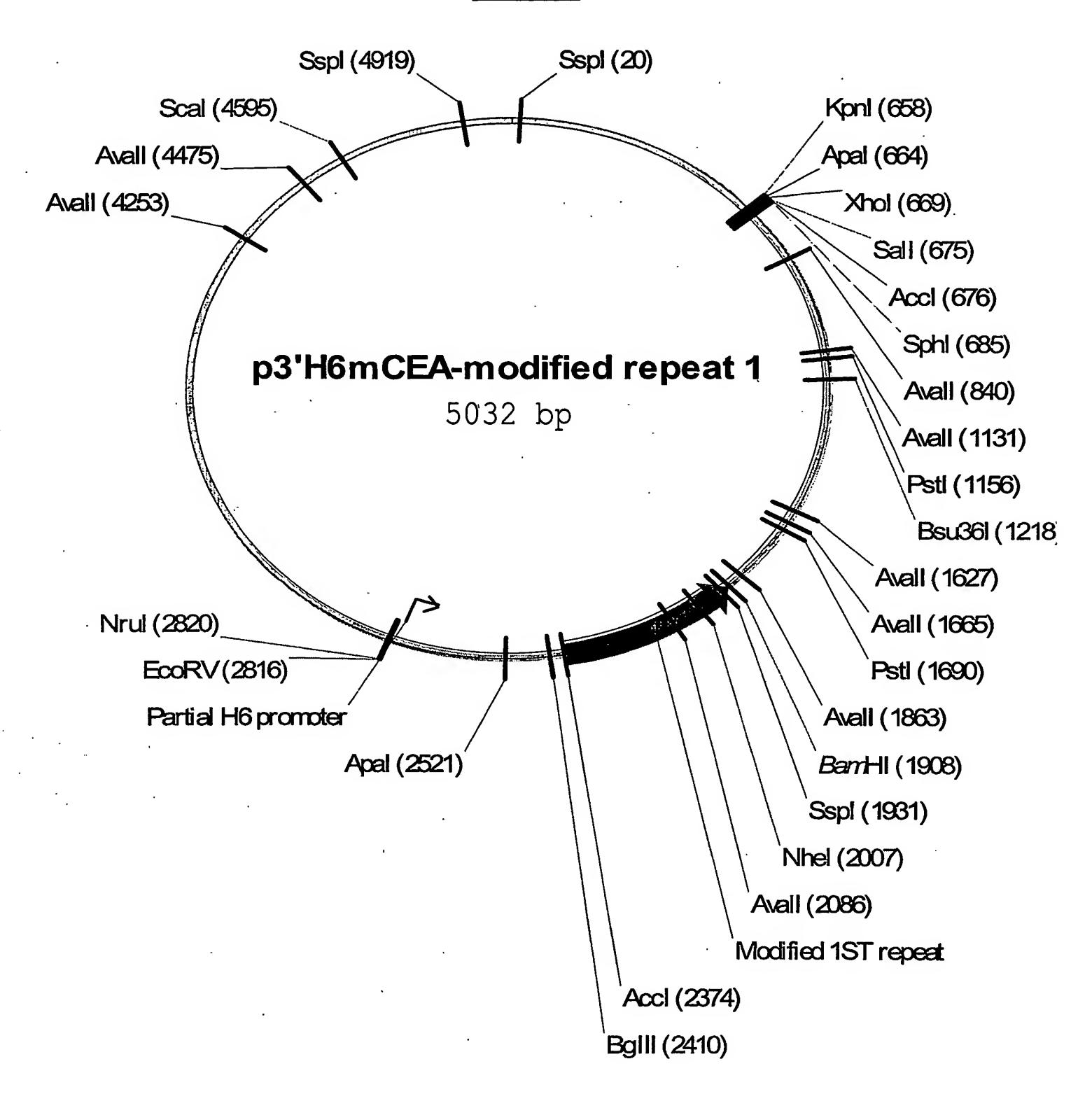
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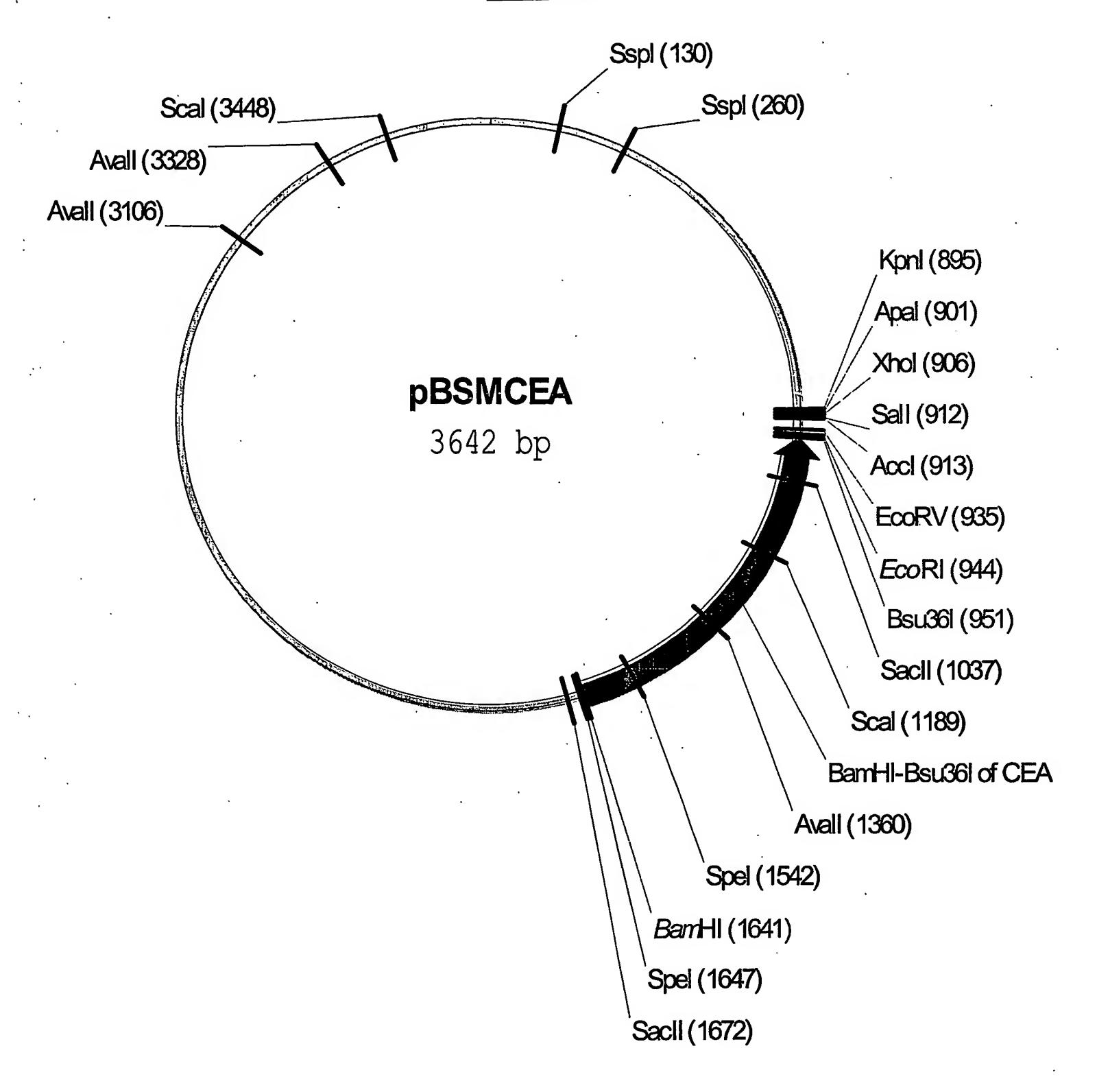


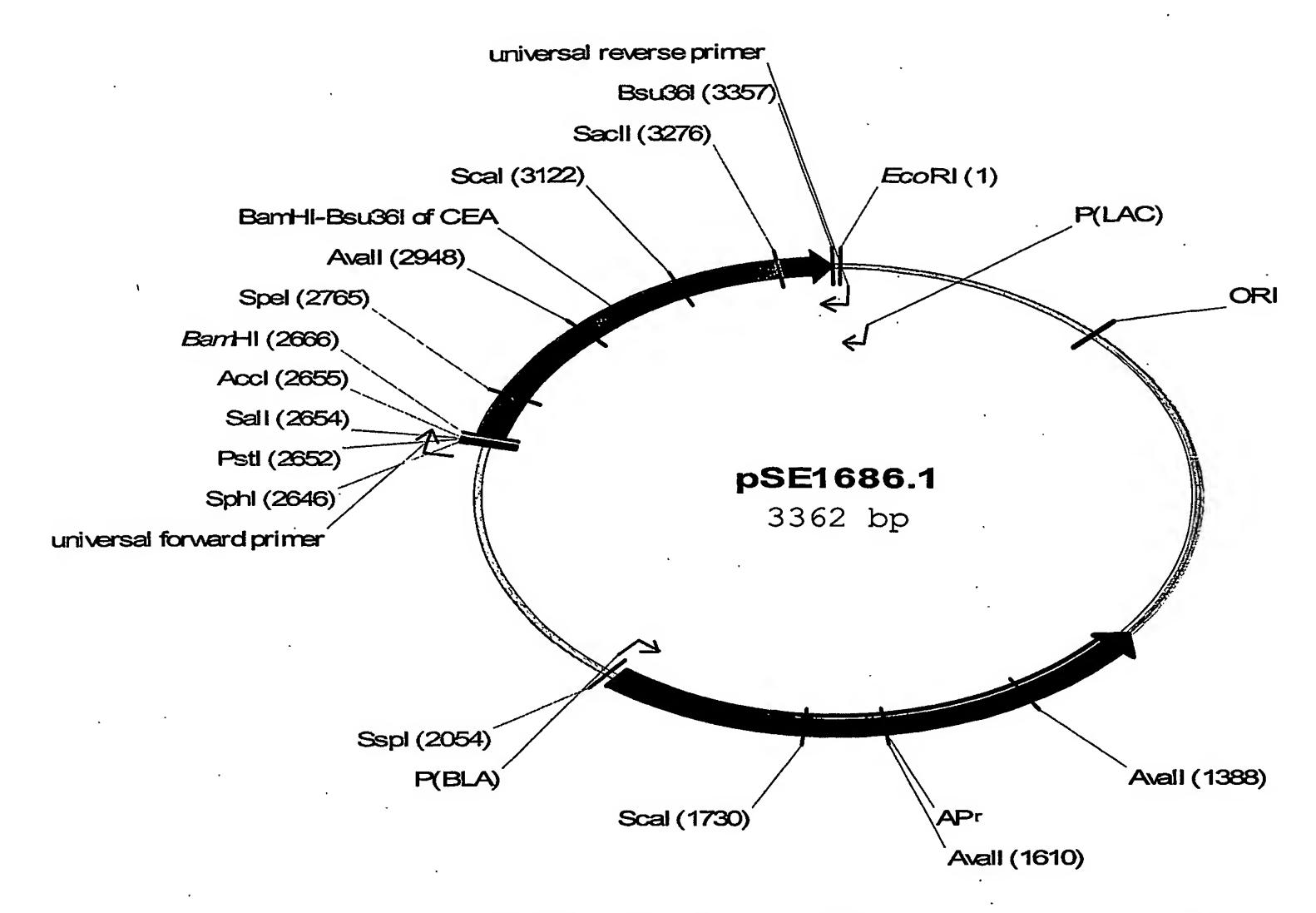




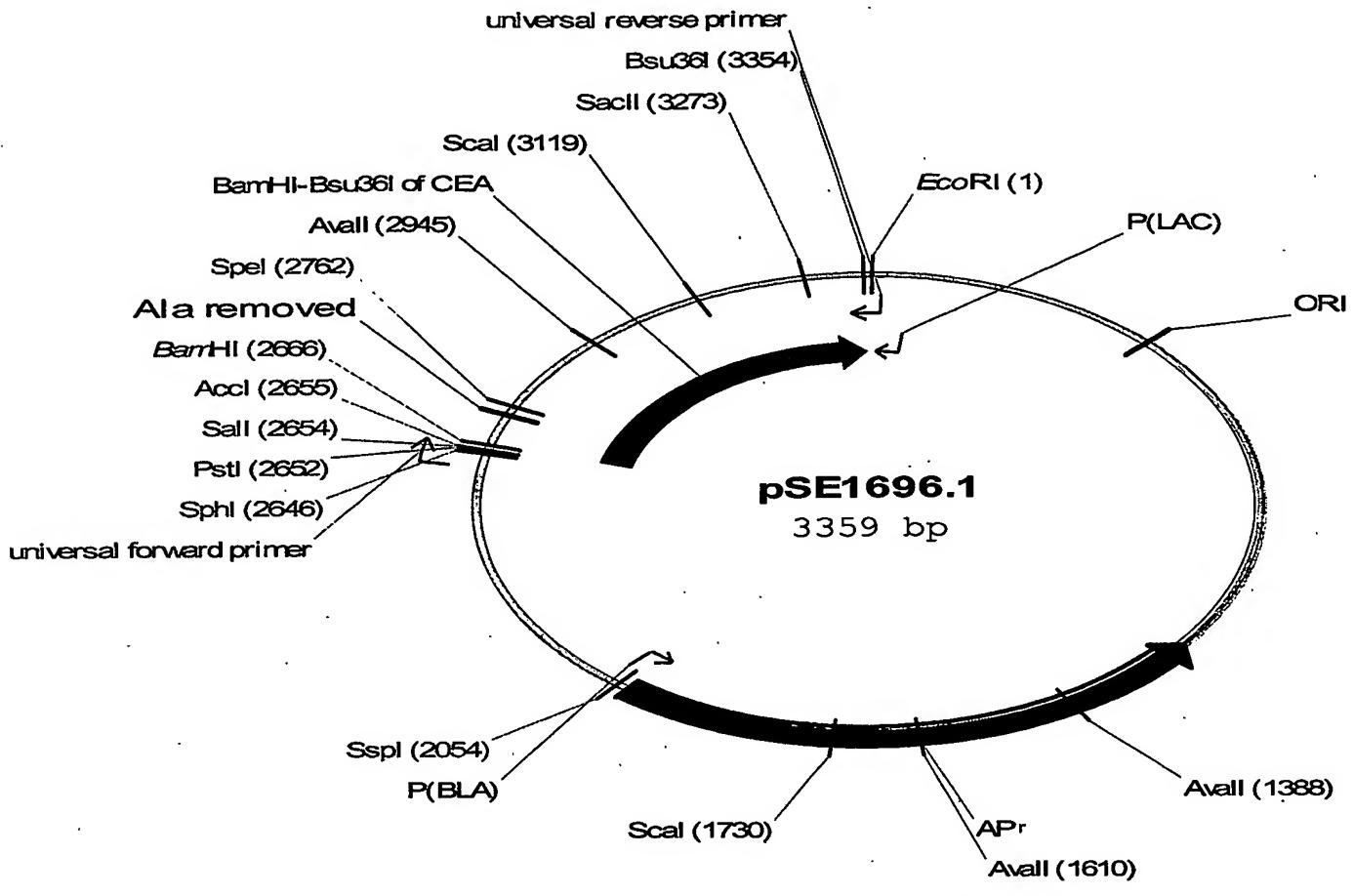
Fragment of annealed oligos modified repeat 1 471 bp



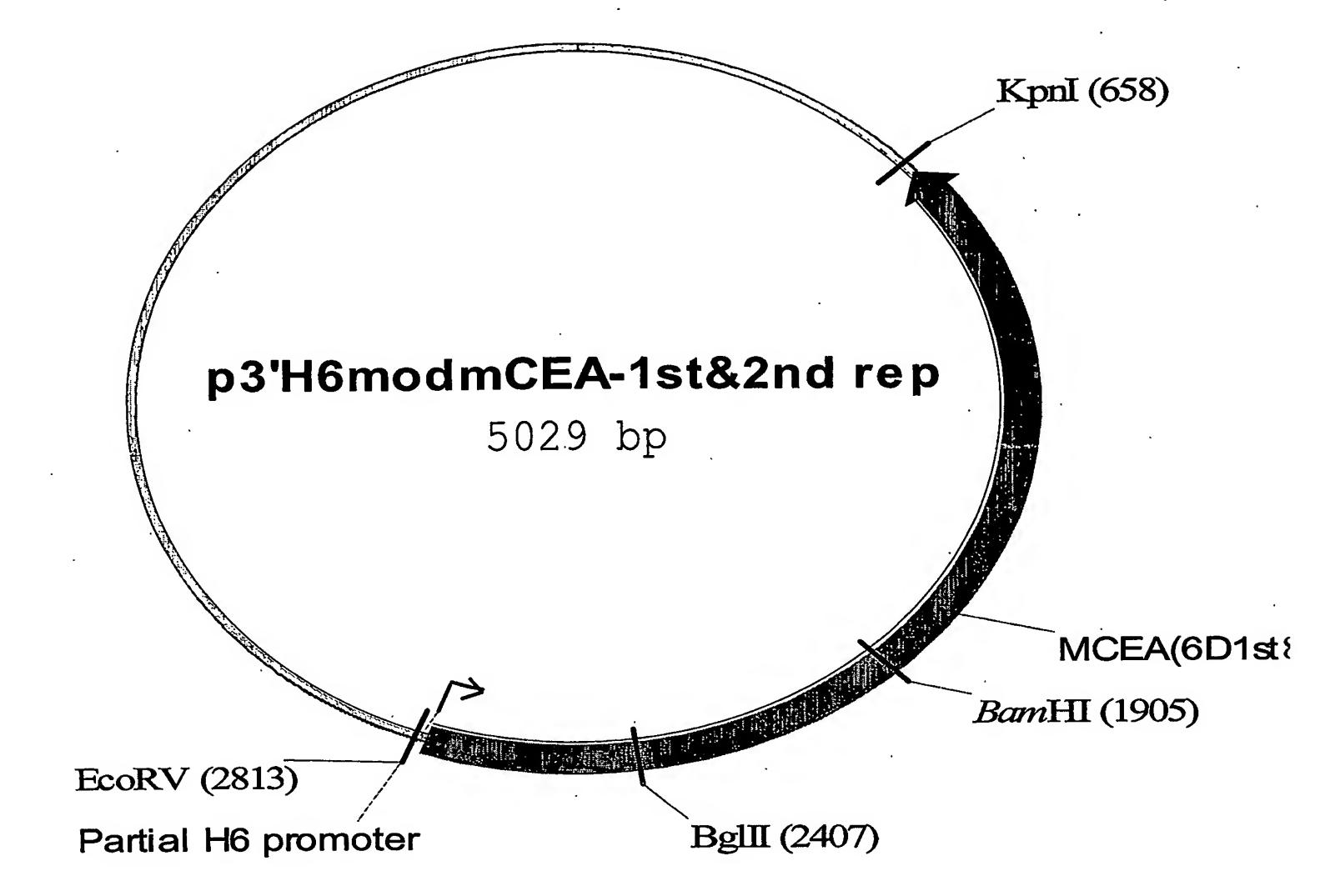




pUC18 mCEA modified repeat 2 (gsoe)



pUC18 mCEA modified repeat 2 gsoe minus Ala



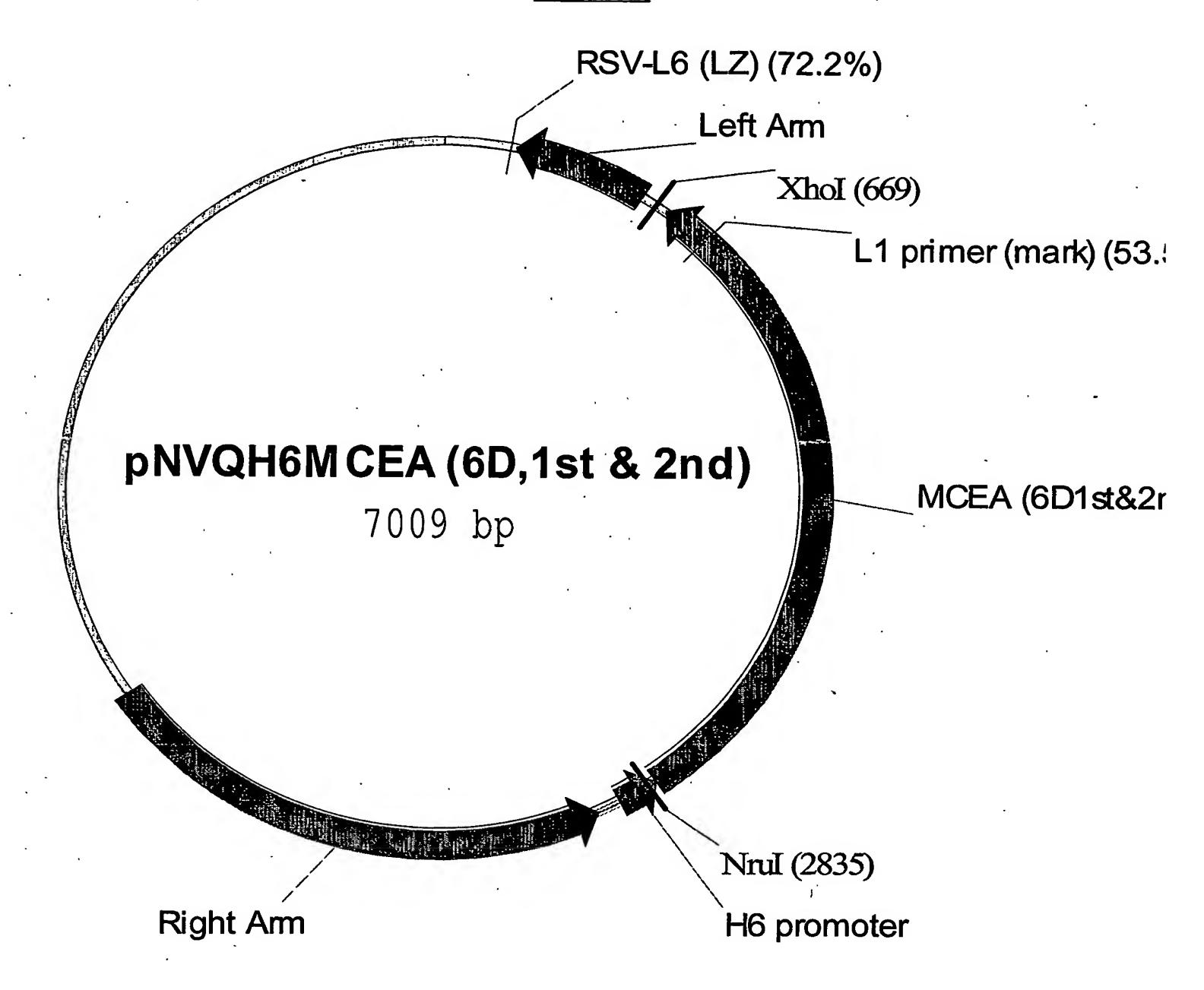


FIGURE 9A

5	mCEA(6D) mCEA(6D,1st&2nd)	1 ATGGAGTCTC ATGGAGTCTC	CCTCGGCCCC			
10	mCEA(6D) mCEA(6D,1st&2nd)	51 GCTCCTGCTC GCTCCTGCTC	ACAGCCTCAC ACAGCCTCAC	·	CTGGAACCCG CTGGAACCCG	100 CCCACCACTG CCCACCACTG
10	mCEA(6D) mCEA(6D,1st&2nd)	101 CCAAGCTCAC CCAAGCTCAC			ATGTCGCAGA ATGTCGCAGA	
15	mCEA(6D) mCEA(6D,1st&2nd)	151 GTGCTTCTAC GTGCTTCTAC	TTGTCCACAA TTGTCCACAA		CATCTTTTTG CATCTTTTTG	200 GCTACAGCTG GCTACAGCTG
20	mCEA(6D) mCEA(6D,1st&2nd)	201 GTACAAAGGT GTACAAAGGT	GAAAGAGTGG GAAAGAGTGG	ATGGCAACCG ATGGCAACCG		250 GGATATGTAA GGATATGTAA
25	mCEA(6D) mCEA(6D,1st&2nd)	251 TAGGAACTCA TAGGAACTCA			CATACAGTGG CATACAGTGG	300 TCGAGAGATA TCGAGAGATA
	mCEA(6D) mCEA(6D,1st&2nd)	301 ATATACCCCA ATATACCCCA			AACATCATCC AACATCATCC	•
30	mCEA(6D) mCEA(6D,1st&2nd)	351 AGGATTCTAC AGGATTCTAC				400 AATGAAGAAG AATGAAGAAG
35	mCEA(6D) mCEA(6D,1st&2nd)	401 CAACTGGCCA CAACTGGCCA		TACCCGGAGC TACCCGGAAC	TGCCCAAGCC TCCCTAAGCC	450 CTCCATCTCC TTCTATTAGC
40	mCEA(6D) mCEA(6D,1st&2nd)	451 AGCAACAACT TCCAATAATA	CCAAACCCGT GTAAGCCTGT	GGAGGACAAG CGAAGACAAA		. 500 CCTTCACCTG CTTTTACATG
45	mCEA(6D) mCEA(6D,1st&2nd)	501 TGAACCTGAG CGAGCCCGAA				
50	mCEA(6D) mCEA(6D,1st&2nd)	551 GCCTCCCGGT CCCTGCCTGT.				600 CAGGACCCTC TAGAACTCTG
50	mCEA(6D) mCEA(6D,1st&2nd)	601 ACTCTATTCA ACCCTGTTTA				

FIGURE 9B

5	mCEA(6D) mCEA(6D,1st&2nd)	651 CCAGAACCCA CCAAAATCCA	GTGAGTGCCA GT <u>C</u> AG <u>C</u> GCCA		TTCAGTCATC TTCAGTGATT	700 CTGAATGTCC CT <u>CAAC</u> GT <u>G</u> C
	mCEA(6D) mCEA(6D,1st&2nd)	701 TCTATGGCCC T <u>T</u> TA <u>C</u> GG <u>A</u> CC		ACCATTTCCC ACAATCAGCC	CTCTAAACAC	
10	mCEA(6D) mCEA(6D,1st&2nd)	751 TCAGGGGAAA TCAGGGGAAA	ATCTGAACCT ATCTGAA <u>T</u> CT	CTCCTGCCAC GAGCTGTCAT	GCAGCCTCTA GCCGCTAGCA	
15	mCEA(6D) mCEA(6D,1st&2nd)	801 ACAGTACTCT CCAATACAGC	TGGTTTGTCA TGGTTTGTCA	ATGGGACTTT ATGG <u>C</u> ACTTT	CCAGCAATCC.	
20	mCEA(6D) mCEA(6D,1st&2nd)	851 TCTTTATCCC TGTTCATTCC	CAACATCACT CAATATTACC	GTGAATAATA GTGAA <u>C</u> AATA	GTGGATCCTA GTGGATCCTA	900 TACGTGCCAA CACGTGCCAA
	mCEA(6D) mCEA(6D, 1st&2nd)	901 GCCCATAACT GCTCACAATA	CAGACACTGG GCGACACCGG		ACCACAGTCA ACAACCGTGA	-,
25	mCEA(6D) mCEA(6D,1st&2nd)	951 AGTCTATGAG CGTGTATGAG	CCACCCAAAC CCACC <u>A</u> AAAC		CAGCAACAAC TAGTAACAAT	1000 TCCAACCCCG TCTAACCCAG
30	mCEA(6D) mCEA(6D,1st&2nd)	1001 TGGAGGATGA TTGAGGATGA	GGATGCTGTA GGACGCAGTT	GCCTTAACCT GCATTAACTT	GTGAACCTGA GTGAGCCAGA	1050 GATTCAGAAC GATTC <u>AA</u> AAT
35	mCEA(6D) mCEA(6D,1st&2nd)	1051 ACAACCTACC ACCACTTATT	TGTGGTGGGT TATGGTGGGT	AAATAATCAG CAATAACCAA	AGCCTCCCGG AGTTTGCCGG	1100 TCAGTCCCAG TTAGCCCACG
40	mCEA(6D) mCEA(6D,1st&2nd)	1101 GCTGCAGCTG CTTGCAGTTG	TCCAATGACA TCTAATGATA		CACTCTACTC GACACTCCTG	•
	mCEA(6D) mCEA(6D,1st&2nd)	1151 GGAATGATGT GCAATGATGT	AGGACCCTAT AGGACCTTAT		TCCAGAACGA TTCAGAATGA	
45	mCEA(6D) mCEA(6D,1st&2nd)		ACCCAGTCAT ACCCTGTTAT		CTCTATGGCC TTGTATGGCC	
50	mCEA(6D) mCEA(6D,1st&2nd)	1251 CACCATTTCC AACTATATCT	CCCTCATACA CCATCATACA	CCTATTACCG CCTACTACCG	TCCAGGGGTG TCCCGGCGTG	1300 AACCTCAGCC AAC <u>T</u> TGAGCC

FIGURE 9C

5	mCEA(6D) mCEA(6D,1st&2nd)	1301 TCTCCTGCCA TTTCTTGCCA		AACCCACCTG AACCCCCCTG	CACAGTATTC CACAGTACTC	1350 TTGGCTGATT CTGGCTGATT
J	mCEA(6D) mCEA(6D,1st&2nd)	1351 GATGGGAACA GATGG <u>A</u> AACA	TCCAGCAACA		CTCTTTATCT TTATTTATAA	1400 CCAACATCAC GCAACATAAC
10	mCEA(6D) mCEA(6D,1st&2nd)			ATACCTGCCA ATAC <u>T</u> TGCCA	_	1450 TCAGCCAGTG TCAGCCAGTG
15	mCEA(6D) mCEA(6D,1st&2nd)	1451 GCCACAGCAG G <u>T</u> CACAGCAG		AAGACAATCA AAAACAATAA		1500 GGAGCTGCCC GGAGCTGCCC
20	mCEA(6D) mCEA(6D,1st&2nd)	1501 AAGCCCTCCA AAGCCCTCCA	_ _ _ _ _ _ _ _ _ _ _ _ _ _ _ 			1550 ACAAGGATGC ACAAGGATGC
25	mCEA(6D) mCEA(6D,1st&2nd)			CTGAGGCTCA CTGAGGCTCA		
20	mCEA(6D) mCEA(6D,1st&2nd)	1601 GGGTAAATGG GGGTAAATGG		-CCAGTCAGTC CCAGTCAGTC		
30	mCEA(6D) mCEA(6D,1st&2nd)			ATTCAATGTC ATTCAATGTC		
35	mCEA(6D) mCEA(6D,1st&2nd)	1701 CTATGTATGT CTATGTATGT		ACTCAGTGAG ACTCAGTGAG	TGCAAACCGC TGCAAACCGC	
40	mCEA(6D) mCEA(6D,1st&2nd)	1751 TCACCCTGGA TCACCCTGGA	TGTCCTCTAT TGTCCTCTAT	GGGCCGGACA GGGCCGGACA		1800 TTCCCCCCCA TTCCCCCCCA
45	mCEA(6D) mCEA(6D,1st&2nd)			AGCGGACCTC AGCGGACCTC		<u>-</u>
	mCEA(6D) mCEA(6D,1st&2nd)			ATTCTTGGCG ATTCTTGGCG		
50	mCEA(6D) mCEA(6D,1st&2nd)			ATCGĆCAAAA ATCGCCAAAA		1950 TAATAACGGG TAATAACGGG

FIGURE 9D

		1951	•	••		2000
	mCEA(6D)	ACCTATGCCT	GTTTTGTCTC	TAACTTGGCT	ACTGGCCGCA	ATAATTCCAT
5	mCEA(6D,1st&2nd)	ACCTATGCCT	GTTTTGTCTC	TAACTTGGCT	ACTGGCCGCA	ATAATTCCAT
		2001		•		2050
	mCEA (6D)	AGTCAAGAGC	ATCACAGTCT	CTGCATCTGG	AACTTCTCCT	GGTCTCTCAG
10	mCEA(6D,1st&2nd)	AGTCAAGAGC	ATCACAGTCT	CTGCATCTGG	AACTTCTCCT	GGTCTCTCAG
10		2051		•		2100
	mCEA(6D)	CTGGGGCCAC	TGTCGGCATC	ATGATTGGAG	TGCTGGTTGG	GGTTGCTCTG
	mCEA(6D,1st&2nd)	CTGGGGCCAC	TGTCGGCATC	ATGATTGGAG	TGCTGGTTGG	GGTTGCTCTG
15		2101			•	
	mCEA (6D)	ATATAG		•		
	mCEA(6D, 1st&2nd)	ATATAG		•		

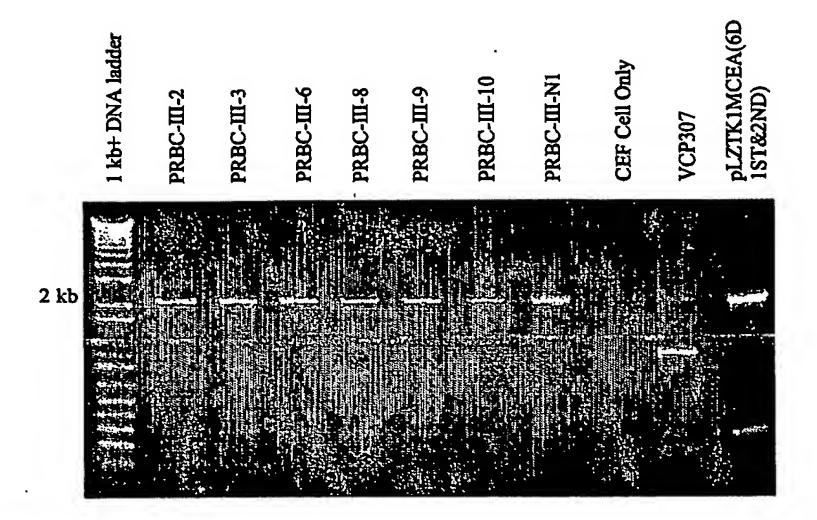
WO 2005/035773 PCT/US2004/033145

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FIGURE 10

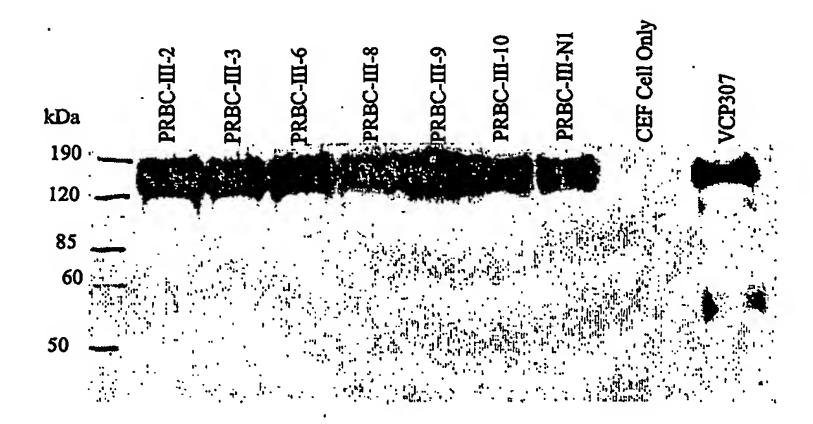
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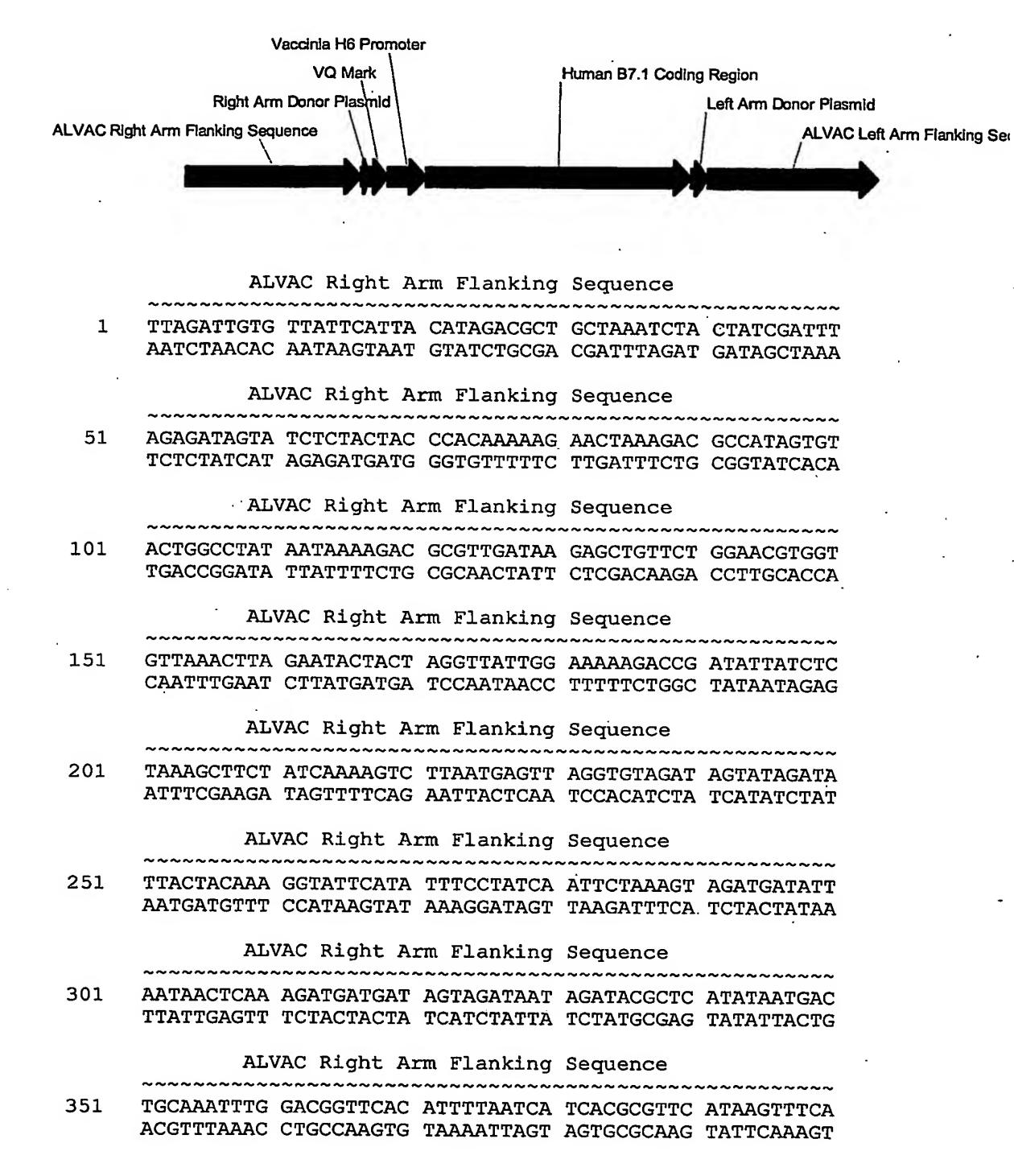
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FIGURE 11

5



10



	AL7	VAC Right A	rm Flanking	Sequence		
401 .			ACTAAAAAGA TGATTTTTCT	•		•
	7JA	VAC Right A	rm Flanking	Sequence	~~~~~~~~~	
451		•	TAAAGAAATŢ ATTTCTTTAA	•		
	AL7	VAC Right A	rm Flanking	Sequence	~~~~~~~	
501			TTATATTTAA AATATAAATT	_ ·		
				Right Arm	Donor Plasm	id
	ALVAC Right	Arm Flank	ing Sequence	e ~~		
551	AAAATAAAT TTTTATTTA _,	ATACTTACTT TATGAATGAA	ACGAAAAAAT TGCTTTTTTA	GACTAATTAG CTGATTAATC		
	~~~~	.~~~~~~~	VQ Mark	~~~~~~~~~	~~~~~~	
	Right Arm I	Donor Plasm:	id			
601			TTAGACAAGG AATCTGTTCC	· — <del>-</del>		
	VQ Mar	ck		•		
	VQ Mar	ck 	Vaccinia	H6 Promote		
651	GCTTAATTAA	~~~~ ~~~ TTAGAGCTTC	Vaccinia ~~~~~~~ TTTATTCTAT AAATAAGATA	ACTTAAAAAG	TGAAAATAAA	
651	GCTTAATTAA	TTAGAGCTTC AATCTCGAAG	TTTATTCTAT	ACTTAAAAAG TGAATTTTTC	TGAAAATAAA	
651 701	GCTTAATTAA CGAATTAATT	TTAGAGCTTC AATCTCGAAG  Vaccini	TTTATTCTAT AAATAAGATA	ACTTAAAAAG TGAATTTTTC er GAAAGCGAGA	TGAAAATAAA ACTTTTATTT  AATAATCATA	
	GCTTAATTAA CGAATTAATT  ~~~~~~~~ TACAAAGGTT ATGTTTCCAA	TTAGAGCTTC AATCTCGAAG  Vaccini	TTTATTCTAT AAATAAGATA ia H6 Promot GTGTTAAATT CACAATTTAA	ACTTAAAAAG TGAATTTTTC er GAAAGCGAGA CTTTCGCTCT	TGAAAATAAA ACTTTTATTT  AATAATCATA	Region
	GCTTAATTAA CGAATTAATT  TACAAAGGTT ATGTTTCCAA	TTAGAGCTTC AATCTCGAAG  Vaccini CTTGAGGGTT GAACTCCCAA	TTTATTCTAT AAATAAGATA ia H6 Promot GTGTTAAATT CACAATTTAA  Promoter	ACTTAAAAAG TGAATTTTTC er GAAAGCGAGA CTTTCGCTCT Human	TGAAAATAAA ACTTTTATTT  AATAATCATA TTATTAGTAT  B7.1 Coding	Region
701	GCTTAATTAA CGAATTAATT  TACAAAGGTT ATGTTTCCAA	TTAGAGCTTC AATCTCGAAG  Vaccini CTTGAGGGTT GAACTCCCAA  Vaccinia H6	TTTATTCTAT AAATAAGATA ia H6 Promot GTGTTAAATT CACAATTTAA	ACTTAAAAAG TGAATTTTTC er GAAAGCGAGA CTTTCGCTCT Human	TGAAAATAAA ACTTTTATTT  AATAATCATA TTATTAGTAT  B7.1 Coding ~~~~~~	Region
701	GCTTAATTAA CGAATTAATT  TACAAAGGTT ATGTTTCCAA	TTAGAGCTTC AATCTCGAAG  Vaccini CTTGAGGGTT GAACTCCCAA  Vaccinia H6 TTATCGCGAT AATAGCGCTA	TTTATTCTAT AAATAAGATA ia H6 Promot GTGTTAAATT CACAATTTAA  Promoter ATCCGTTAAG	ACTTAAAAAG TGAATTTTTC er GAAAGCGAGA CTTTCGCTCT Human TTTGTATCGT AAACATAGCA	TGAAAATAAA ACTTTTATTT  AATAATCATA TTATTAGTAT  B7.1 Coding ~~~~~~	Region
701	GCTTAATTAA CGAATTAATT  TACAAAGGTT ATGTTTCCAA  AATTATTTCA TTAATAAAGT  ACACGGAGGC	TTAGAGCTTC AATCTCGAAG  Vaccinia CTTGAGGGTT GAACTCCCAA  TTATCGCGAT AATAGCGCTA  Human B7. AGGGAACATC	TTTATTCTAT AAATAAGATA ia H6 Promot GTGTTAAATT CACAATTTAA  Promoter ATCCGTTAAG TAGGCAATTC	ACTTAAAAAG TGAATTTTTC er GAAAGCGAGA CTTTCGCTCT Human TTTGTATCGT AAACATAGCA egion TGTCCATACC	TGAAAATAAA ACTTTTATTT  AATAATCATA TTATTAGTAT  B7.1 Coding ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	Region
701	GCTTAATTAA CGAATTAATT  TACAAAGGTT ATGTTTCCAA  AATTATTTCA TTAATAAAGT  ACACGGAGGC	TTAGAGCTTC AATCTCGAAG  Vaccinia CTTGAGGGTT GAACTCCCAA  ACCINIA H6 TTATCGCGAT AATAGCGCTA  Human B7. AGGGAACATC TCCCTTGTAG	TTTATTCTAT AAATAAGATA  ia H6 Promot GTGTTAAATT CACAATTTAA  Promoter ATCCGTTAAG TAGGCAATTC  1 Coding Re ACCATCCAAG	ACTTAAAAAG TGAATTTTTC er GAAAGCGAGA CTTTCGCTCT Human  TTTGTATCGT AAACATAGCA egion TGTCCATACC ACAGGTATGG	TGAAAATAAA ACTTTTATTT  AATAATCATA TTATTAGTAT  B7.1 Coding ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	Region

	Human B7.1 Coding Region
901	ACGTGACCAA GGAAGTGAAA GAAGTGGCAA CGCTGTCCTG TGGTCACAAT TGCACTGGTT CCTTCACCTTT CTTCACCGTT GCGACAGGAC ACCAGTGTTA
	Human B7.1 Coding Region
951	GTTTCTGTTG AAGAGCTGGC ACAAACTCGC ATCTACTGGC AAAAGGAGAA CAAAGACAAC TTCTCGACCG TGTTTGAGCG TAGATGACCG TTTTCCTCTT
	Human B7.1 Coding Region
1001	GAAAATGGTG CTGACTATGA TGTCTGGAGA CATGAATATA TGGCCCGAGT CTTTTACCAC GACTGATACT ACAGACCTCT GTACTTATAT ACCGGGCTCA
	Human B7.1 Coding Region
1051	ACAAGAACCG GACCATCTTT GATATCACTA ATAACCTCTC CATTGTGATC TGTTCTTGGC. CTGGTAGAAA CTATAGTGAT TATTGGAGAG GTAACACTAG
	Human B7.1 Coding Region
1101	CTGGCTCTGC GCCCATCTGA CGAGGGCACA TACGAGTGTG TTGTTCTGAA GACCGAGACG CGGGTAGACT GCTCCCGTGT ATGCTCACAC AACAAGACTT
	Human B7.1 Coding Region
1151	GTATGAAAAA GACGCTTTCA AGCGGGAACA CCTGGCTGAA GTGACGTTAT CATACTTTTT CTGCGAAAGT TCGCCCTTGT GGACCGACTT CACTGCAATA
	Human B7.1 Coding Region
1201	CAGTCAAAGC TGACTTCCCT ACACCTAGTA TATCTGACTT TGAAATTCCA GTCAGTTTCG ACTGAAGGGA TGTGGATCAT ATAGACTGAA ACTTTAAGGT
	Human B7.1 Coding Region
1251	ACTTCTAATA TTAGAAGGAT AATTTGCTCA ACCTCTGGAG GTTTTCCAGA TGAAGATTAT AATCTTCCTA TTAAACGAGT TGGAGACCTC CAAAAGGTCT
	Human B7.1 Coding Region
1301	GCCTCACCTC TCCTGGTTGG AAAATGGAGA AGAATTAAAT GCCATCAACA CGGAGTGGAG AGGACCAACC TTTTACCTCT TCTTAATTTA CGGTAGTTGT
	Human B7.1 Coding Region
1351	CAACAGTTTC CCAAGATCCT GAAACTGAGC TCTATGCTGT TAGCAGCAAA GTTGTCAAAG GGTTCTAGGA CTTTGACTCG AGATACGACA ATCGTCGTTT
	Human B7.1 Coding Region
1401	CTGGATTTCA ATATGACAAC CAACCACAGC TTCATGTGTC TCATCAAGTA GACCTAAAGT TATACTGTTG GTTGGTGTCG AAGTACACAG AGTAGTTCAT

	Human B7.1 Coding Region
1451	TGGACATTTA AGAGTGAATC AGACCTTCAA CTGGAATACA ACCAAGCAAG ACCTGTAAAT TCTCACTTAG TCTGGAAGTT GACCTTATGT TGGTTCGTTC
	Human B7.1 Coding Region
1501	AGCATTTTCC TGATAACCTG CTCCCATCCT GGGCCATTAC CTTAATCTCA TCGTAAAAGG ACTATTGGAC GAGGGTAGGA CCCGGTAATG GAATTAGAGT
	Human B7.1 Coding Region
1551	GTAAATGGAA TTTTCGTGAT ATGCTGCCTG ACCTACTGCT TTGCCCCACG CATTTACCTT AAAAGCACTA TACGACGGAC TGGATGACGA AACGGGGTGC
	Human B7.1 Coding Region
1601	CTGCAGAGAG AGAAGGAGGA ATGAGAGATT GAGAAGGGAA AGTGTACGTC GACGTCTCTC TCTTCCTCT TACTCTCTAA CTCTTCCCTT TCACATGCAG
	Left Arm Donor Plasmid
	Human B7.1 Coding Region
1651	CTGTATAATT TTTATCTCGA GCCCGGGAAG CTTGAATTCT TTTTATTGAT GACATATTAA AAATAGAGCT CGGGCCCTTC GAACTTAAGA AAAATAACTA
	ALVAC Left Arm Flanking Sequence
	Left Arm Donor Plasmid
1701	TAACTAGTCA AATGAGTATA TATAATTGAA AAAGTAAAAT ATAAATCATA ATTGATCAGT TTACTCATAT ATATTAACTT TTTCATTTTA TATTTAGTAT
	ALVAC Left Arm Flanking Sequence
1751	TAATAATGAA ACGAAATATC AGTAATAGAC AGGAACTGGC AGATTCTTCT ATTATTACTT TGCTTTATAG TCATTATCTG TCCTTGACCG TCTAAGAAGA
	ALVAC Left Arm Flanking Sequence
1801	TCTAATGAAG TAAGTACTGC TAAATCTCCA AAATTAGATA AAAATGATAC AGATTACTTC ATTCATGACG ATTTAGAGGT TTTAATCTAT TTTTACTATG
-	ALVAC Left Arm Flanking Sequence
1851	AGCAAATACA GCTTCATTCA ACGAATTACC TTTTAATTTT TTCAGACACA TCGTTTATGT CGAAGTAAGT TGCTTAATGG AAAATTAAAA AAGTCTGTGT
	ALVAC Left Arm Flanking Sequence
1901	CCTTATTACA AACTAACTAA GTCAGATGAT GAGAAAGTAA ATATAAATTT GGAATAATGT TTGATTGATT CAGTCTACTA CTCTTTCATT TATATTTAAA

~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
1951 AACTTATGGG TATAATAA TAAAGATTCA TGATATTAAT AATTTACTT
TTGAATACCC ATATTATATT ATTTCTAAGT ACTATAATTA TTAAATGAA
•
ALVAC Left Arm Flanking Sequence
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
2001 ACGATGTTAA TAGACTTATT CCATCAACCC CTTCAAACCT TTCTGGATA
TGCTACAATT ATCTGAATAA GGTAGTTGGG GAAGTTTGGA AAGACCTAT
•
ALVAC Left Arm Flanking Sequence
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
2051 TATAAAATAC CAGTTAATGA TATTAAAATA GATTGTTTAA GAGATGTAA
ATATTTATG GTCAATTACT ATAATTTTAT CTAACAAATT CTCTACATT
, and the state of
ALVAC Left Arm Flanking Sequence
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
2101 TAATTATTTG GAGGTAAAGG ATATAAAATT AGTCTATCTT TCACATGGA
ATTAATAAAC CTCCATTTCC TATATTTTAA TCAGATAGAA AGTGTACCT
. ATTANTAMO CICCATITOC TATATITTAA TOAGATAGAA AGIGTACOT
ALVAC Left Arm Flanking Sequence
ADVAC DELC AIM FIGHKING DEQUENCE
2151 ATGAATTACC TAATATTAAT AATTATGATA GGAATTTTTT AGGATTTAC
TACTTAATGG ATTATAATTA TTAATACTAT CCTTAAAAAA TCCTAAATG
IACITATIGG ATTATATTA TTAATACTAT CCTTAAAAAA TCCTAAATG
ATMAC Toft Arm Flanking Coguenge
ALVAC Left Arm Flanking Sequence
2201 GCTGTTATAT GTATCAACAA TACAGGCAGA TCTATGGTTA TGGTAAAAC
CGACAATATA CATAGTTGTT ATGTCCGTCT AGATACCAAT ACCATTTTG
ATTIAC Total Arm Elevision Company
ALVAC Left Arm Flanking Sequence
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
2251 CTGTAACGGG AAGCAGCAT
GACATTGCCC TTCGTCGTA



	C3R Arm
L	ATATTATTAA AACTATTAGA TAACATAGCT TTATGTAAAG GAGTATTTCC
	TATAATAATT TTGATAATCT ATTGTATCGA AATACATTTC CTCATAAAGG
	C3R Arm
	AGATAACTTA GCTTTAGCAT TTACGTAAGC ACCGTGGTCA AGTAAGAGTT
	TCTATTGAAT CGAAATCGTA AATGCATTCG TGGCACCAGT TCATTCTCAA
	C3R Arm
	TAACAAATTC TGTTTTCATA GAACTAACTG CCATGTATAG AGGAGTGAAA
	ATTGTTTAAG ACAAAAGTAT CTTGATTGAC GGTACATATC TCCTCACTTT
	C3R Arm
	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
	CCTTTATGAT TATAGACGTT TACATAGCAA CCATATAATA AGATCGCATT
	GGAAATACTA ATATCTGCAA ATGTATCGTT GGTATATTAT TCTAGCGTAA
	C3R Arm
	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
	CAGTATATTA ATATCTTTCA TTTCTATAGC TATGTGAATA ACATGTTTAT
	GTCATATAAT TATAGAAAGT AAAGATATCG ATACACTTAT TGTACAAATA
	C3R Arm
	\sim
	CTAATCCTAC CAACTTTGTA TCAGTACCGT ACTTCAGTAA TAAGTTTACT GATTAGGATG GTTGAAACAT AGTCATGGCA TGAAGTCATT ATTCAAATGA
	GATIAGGAIG GIIGAAACAI AGICAIGGCA IGAAGICAII AIICAAAIGA
	C3R Arm
	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
	ATAGTTTTGT TTTTAGATGC AACAGCTATA TTTAGAACGG TATCTATATG
	TATCAAAACA AAAATCTACG TTGTCGATAT AAATCTTGCC ATAGATATAC

.

	C3R Arm
351	ATTATTAACC ACATTAACAT TAGATCCTCT TTCTAAAAGT GTCTTTGTTG TAATAATTGG TGTAATTGTA ATCTAGGAGA AAGATTTTCA CAGAAACAAC C3R Arm
401	TTTCGATATC GTTACGTGAA ACAGCGTAAT GTAAGGGACT GCCCATACAG AAAGCTATAG CAATGCACTT TGTCGCATTA CATTCCCTGA CGGGTATGTC
	C3R Arm
451	TCATCTATTA CGTTTATATC AGCTCCTAGA TTTAACAGAA GTGCTGTTAC AGTAGATAAT GCAAATATAG TCGAGGATCT AAATTGTCTT CACGACAATG
	. C3R Arm
501	ATCTTTTCTT CTATTAATTA CCGAATGATG TAATGGGGTT TTACCTAAAT TAGAAAAGAA GATAATTAAT GGCTTACTAC ATTACCCCAA AATGGATTTA
	C3R Arm
551	CATCTTGTTC GTTTATAGGC ACTCCGTGAT TTATAAGTAA CGCTATTATA GTAGAACAAG CAAATATCCG TGAGGCACTA AATATTCATT GCGATAATAT
	C3R Arm
601	TCGTAACTAC AATTATTTTT AAGTGCCTTT ATGAGATACT GTTTATGCAA AGCATTGATG TTAATAAAAA TTCACGGAAA TACTCTATGA CAAATACGTT
	C3R Arm
651	AAATAAACTT TTATCTATTT TAATACTATT ATCTAACAAT ATCCTAATTA TTTATTTGAA AATAGATAAA ATTATGATAA TAGATTGTTA TAGGATTAAT
	C3R Arm
701	AATCTATATT CTTATACTTT ATAGCGTAAT GTAACGGAGT TTCAAAATTT TTAGATATAA GAATATGAAA TATCGCATTA CATTGCCTCA AAGTTTTAAA
	C3R Arm
751	CTAGTTTGTA TATTAAGATC AATATTAAAA TCTATAAATA TTTTATACAT GATCAAACAT ATAATTCTAG TTATAATTTT AGATATTTAT AAAATATGTA
	C3R Arm
801	ATCATCAGAT ATCTTATCAT ACAGTACATC GTAATAATTT AGAAAGAATC TAGTAGTCTA TAGAATAGTA TGTCATGTAG CATTATTAAA TCTTTCTTAG
	C3R Arm
851	TATTACAATT AACACCTTTT TTTAATAAAT ATCTAGTTAA TGACTTATTG ATAATGTTAA TTGTGGAAAA AAATTATTTA TAGATCAATT ACTGAATAAC

		•	C3R Arm		
901	TTTCTATATA AAAGATATAT	CAGAAATATA GTCTTTATAT		TTTCCAGAAT AAAGGTCTTA	•
		(	C3R Arm		
951		CCAGAATCTA GGTCTTAGAT			GTATTATCTA CATAATAGAT
<b>**</b> **********************************		(	C3R Arm		
1001		TTTATGAAGA AAATACTTCT		TACATTTTAA ATGTAAAATT	AATATCGGCA TTATAGCCGT
	~~~~~~~~	( ~~~~~~~	C3R Arm	~~~~~~~	
1051	CCGTGTTCTA GGCACAAGAT	GTAATAATTT CATTATTAAA	TACCATTTCT		TACTTACGGC
.4	·			TAIAGICITI	AIGAAIGCCG
•	~~~~~~~~	·~~~~~~~~	C3R Arm	·~~~~~~~~	~~~~~~~
1101	TAAATACAAA	GACGTTGATA	GTATATTTAC	GTTATTGTAT	TTGCATTTTT
•	ATTTATGTTT	CTGCAACTAT	CATATAAATG	CAATAACATA	AACGTAAAAA
	~~~~~~~~~	(	C3R Arm		
1151	TAAGTATATA ATTCATATAT	CCTTACTAAA GGAATGATTT	TTTATATCTC AAATATAGAG	TATACCTTAT ATATGGAATA	
			C3R Arm	•	·
1201	AGTTCATTTA TCAAGTAAAT	TAAGTCTTCC ATTCAGAAGG		TCTGGTAATG AGACCATTAC	
			C3R Arm		,
1251	TATCATTATG ATAGTAATAC	ATATTATCTC	TATTTTATTC	TAATAAAAAC ATTATTTTTG	CGTTATCATG
			C3R Arm		
1201		~~~~~~~~~			
1301	TTATTTATTA AATAAATAAT	TTTGTTATAA AAACAATATT	TTATACTATT AATATGATAA	TAATAAATTA ATTATTTAAT	
			C3R Arm	.~~~~~~~	
1351		ATTAATACCA TAATTATGGT	TCCTAGAACT	TGTATTTCTT	GCCCCTAÄA
		C	C3R Arm		
1401		CACTCCATTA GTGAGGTAAT			

	C3R Arm	
1451	TAACATATCC TACTGTTATG TGAGGATTCC ACGGATTATC TACTGTGATA ATTGTATAGG ATGACAATAC ACTCCTAAGG TGCCTAATAG ATGACACTA	_
	C3R Arm	
1501	TCACCAAACA CGTCCTTCGA ACAGGGTACC GCATTCAGCA GAACATTTC	_
	C3R Arm	
1551	TAGGGCTCTA AGTTCATCAG ATACCTCCAG TTTCATAACT ACAGCGCATCATCCCGAGAT TCAAGTAGTC TATGGAGGTC AAAGTATTGA TGTCGCGTAC	_
	C3R Arm	~_
1601	CTTTCGCTCC CAACTGTTTA GAGGCGTTAC TCTGAGGAAA ACACATCTCTGAAAAGCGAGG GTTGACAAAT CTCCGCAATG AGACTCCTTT TGTGTAGAGA	_
	C3R Arm	· <b>-</b>
1651	TCTTTACAGA CTATAGAAAT AGTCTGTAAA TCTTGATCAG TTATTTGCT	~ Ti
1001	AGAAATGTCT GATATCTTTA TCAGACATTT AGAACTAGTC AATAAACGAA	
	C3R Arm	•
1701	TTTGAAATTT TCAAATCTAT CACATTGATC CATATTTGCT ATTCCAAGACAAAACTTTAAA AGTTTAGATA GTGTAACTAG GTATAAACGA TAAGGTTCTC	_
•	. C3R Arm	
1751	TTATATGAGG AAAAATATCA CATCCTGTCA TGTATTTTAT TGTAACATTAAAATAATAATAATAATAATAATAATAATAATA	_
	C3R Arm	L
	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	<u> </u>
1801	TTATAATCTG TAACATCAGT ATCTAACCTA ACGTCGTAAA AGTTAACAGAAAATATTAGAC ATTGTAGTCA TAGATTGGAT TGCAGCATTT TCAATTGTCT	
	C3R Arm	
1851	TGCCCAGTTA CTATAATCCC AAGGAACCTT AACATCTAAT CCCATTAAAA	-
•	ACGGGTCAAT GATATTAGGG TTCCTTGGAA TTGTAGATTA GGGTAATTTT	['
	C3R Arm	-
1901	TAGTATCCTT TCTACTATTT TTTTCATTGG CAAGTATGTG GCTTAGTTTA ATCATAGGAA AGATGATAAA AAAAGTAACC GTTCATACAC CGAATCAAA1	
	C3R Arm	
1951	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	

				H6	5 promoter		
2001				C GGGATCCTTC CCCTAGGAAC	TTTATTCTAT AAATAAGATA		
	~~~~~~~~~	. Н	promoter	•			
2051	ACTTAAAAA( TGAATTTTT(			CTTGAGGGTT	GTGTTAAATT CACAATTTAA		
•	~~~~~~~	H6	promoter				
2101	GAAAGCGAGA				ATCCGTTAAG TAGGCAATTC		
	MCEA						
	H6 promote	er		~~~~~~~	~~~~~~~~~		
2151	TTTGTATCGT AAACATAGCA			GTCCCCACAG GAGGGGTGTC	ATGGTGCATC TACCACGTAG		
			MCEA				
2201	CCCTGGCAGA	GGCTCCTGCT CCGAGGACGA	CACAGCCTCA GTGTCGGAGT	CTTCTAACCT GAAGATTGGA	TCTGGAACCC AGACCTTGGG		
	<b>24 24 24 24 24 24 24 24 24 24 24 24 24 2</b>		MCEA				
2251	GCCCACCACT CGGGTGGTGA	GCCAAGCTCA CGGTTCGAGT	CTATTGAATC GATAACTTAG	CACGCCGTTC GTGCGGCAAG	AATGTCGCAG TTACAGCGTC		
		, •	MCEA				
2301	AGGGGAAGGA TCCCCTTCCT	GGTGCTTCTA CCACGAAGAT	CTTGTCCACA GAACAGGTGT	ATCTGCCCCA TAGACGGGGT	GCATCTTTTT CGTAGAAAAA		
			MCEA		-		
2351	GGCTACAGCT CCGATGTCGA		TGAAAGAGTG ACTTTCTCAC	GATGGCAACC CTACCGTTGG	GTCAAATTAT CAGTTTAATA		
	~~~~~~~~~	·~~~~~~~~~	MCEA	<b></b>			
2401	AGGATATGTA TCCTATACAT	ATAGGAACTC TATCCTTGAG	AACAAGCTAC TTGTTCGATG	CCCAGGGCCC GGGTCCCGGG	GCATACAGTG CGTATGTCAC		
	24 24 24 24 24 24 24 24 24 24 24 24 24 2		MCEA				
2451	GTCGAGAGAT CAGCTCTCTA	AATATACCCC TTATATGGGG	AATGCATCCC TTACGTAGGG	TGCTGATCCA ACGACTAGGT	GAACATCATC CTTGTAGTAG		
	~~~~~		MCEA				
2501	CAGAATGACA GTCTTACTGT	CAGGATTCTA GTCCTAAGAT	CACCCTACAC GTGGGATGTG	GTCATAAAGT CAGTATTTCA	CAGATCTTGT GTCTAGAACA		

	MCEA	
2551	GAATGAAGAA GCAACTGGCC AGTTCCGGGT ATACCCGGAA CTCCCTAAGC CTTACTTCTT CGTTGACCGG TCAAGGCCCA TATGGGCCTT GAGGGATTCG	
	MCEA	
2601	CTTCTATTAG CTCCAATAAT AGTAAGCCTG TCGAAGACAA AGATGCCGTC GAAGATAATC GAGGTTATTA TCATTCGGAC AGCTTCTGTT TCTACGGCAG	
	MCEA	
2651	GCTTTTACAT GCGAGCCCGA AACTCAAGAC GCAACATATC TCTGGTGGGT CGAAAATGTA CGCTCGGGCT TTGAGTTCTG CGTTGTATAG AGACCACCCA	
	MCEA	
2701	GAACAACCAG TCCCTGCCTG TGTCCCCTAG ACTCCAACTC AGCAACGGAA CTTGTTGGTC AGGACGGAC ACAGGGGATC TGAGGTTGAG TCGTTGCCTT	
	MCEA	
2751	ATAGAACTCT GACCCTGTTT AACGTGACCA GGAACGACAC AGCAAGCTAC TATCTTGAGA CTGGGACAAA TTGCACTGGT CCTTGCTGTG TCGTTCGATG	
	MCEA	
2801	AAATGCGAAA CCCAAAATCC AGTCAGCGCC AGGAGGTCTG ATTCAGTGAT TTTACGCTTT GGGTTTTAGG TCAGTCGCGG TCCTCCAGAC TAAGTCACTA	
	MCEA	
2851	TCTCAACGTG CTTTACGGAC CCGATGCTCC TACAATCAGC CCTCTAAACA AGAGTTGCAC GAAATGCCTG GGCTACGAGG ATGTTAGTCG GGAGATTTGT	
	MCEA	
2901	CAAGCTATAG ATCAGGGGAA AATCTGAATC TGAGCTGTCA TGCCGCTAGC GTTCGATATC TAGTCCCCTT TTAGACTTAG ACTCGACAGT ACGGCGATCG	
	MCEA	
2951	AATCCTCCCG CCCAATACAG CTGGTTTGTC AATGGCACTT TCCAACAGTC TTAGGAGGGC GGGTTATGTC GACCAAACAG TTACCGTGAA AGGTTGTCAG	
	MCEA	
3001	CACCCAGGAA CTGTTCATTC CCAATATTAC CGTGAACAAT AGTGGATCCT GTGGGTCCTT GACAAGTAAG GGTTATAATG GCACTTGTTA TCACCTAGGA	
	MCEA	
3051	ACACGTGCCA AGCTCACAAT AGCGACACCG GACTCAACCG CACAACCGTG TGTGCACGGT TCGAGTGTA TCGCTGTGGC CTGAGTTGGC GTGTTGGCAC	

	<b>A.A. </b>		MCEA	.~~~~~~~	
3101	ACGACGATTA TGCTGCTAAT	A CCGTGTATGA CGCACATACI	GCCACCAAAA	CCATTCATAA	CTAGTAACAA
			MCEA	•	
3151	TTCTAACCCA AAGATTGGGI	GTTGAGGATG	AGGACGCAGT TCCTGCGTCA	TGCATTAACT ACGTAATTGA	TGTGAGCCAG ACACTCGGTC
			MCEA		
3201	AGATTCAAAA TCTAAGTTTT	TACCACTTAT ATGGTGAATA	TTATGGTGGG	TCAATAACCA AGTTATTGGT	AAGTTTGCCG TTCAAACGGC
	~~~~~~~~		MCEA	,	
3251		GCTTGCAGTT CGAACGTCAA			
	•		MCEA .		
3301	GTCCGTTACT CAGGCAATGA	CGCAATGATG GCGTTACTAC	TAGGACCTTA	TGAGTGTGGC ACTCACACCG	ATTCAGAATG TAAGTCTTAC
	2422222222222		MCEA		
33 ⁵ 1		TGATCACTCC ACTAGTGAGG			
			MCEA		
3401	CCAGACGACC GGTCTGCTGG	CAACTATATC GTTGATATAG	TCCATCATAC AGGTAGTATG	ACCTACTACC TGGATGATGG	GTCCCGGCGT CAGGGCCGCA
			MCEA		
3451	GAACTTGAGC CTTGAACTCG	CTTTCTTGCC GAAAGAACGG	ATGCAGCATC TACGTCGTAG	CAACCCCCCT GTTGGGGGGA	GCACAGTACT CGTGTCATGA
			MCEA		
3501	CCTGGCTGAT GGACCGACTA	TGATGGAAAC ACTACCTTTG	ATTCAGCAGC TAAGTCGTCG	ATACTCAAGA TATGAGTTCT	GTTATTTATA CAATAAATAT
			MCEA		
3551	AGCAACATAA TCGTTGTATT	CTGAGAAGAA GACTCTTCTT	CAGCGGACTC GTCGCCTGAG	TATACTTGCC ATATGAACGG	AGGCCAATAA TCCGGTTATT
			MCEA		
3601	CTCAGCCAGT GAGTCGGTCA	GGTCACAGCA CCAGTGTCGT			

			MCEA		
3651					ACCCGTGGAG TGGGCACCTC
			MCEA		•
3701					AGAACACAAC TCTTGTGTTG
	242222222222		MCEA		
3751					CCCAGGCTGC
	~~~~~~~~~	~~~~~~~~	MCEA		
3801					CACAAGAAAT GTGTTCTTTA
			MCEA		-
3851					GTGCAAACCG CACGTTTGGC
			MCEA		
3901			ATGTCCTCTA TACAGGAGAT		ACCCCCATCA TGGGGGTAGT
			MCEA		•
3951			TACCTTTCGG ATGGAAAGCC		
	~~~~~~~~~		MCEA		•
4001			ATCCCCGCAG TAGGGGCGTC		
	~~~~~~~~~~		MCEA		
4051		CAACACACAC GTTGTGTGTG	AAGTTCTCTT TTCAAGAGAA	TATCGCCAAA ATAGCGGTTT	
	~~~~~~~~	·~~~~~~~~~~~	MCEA		
4101			TGTTTTGTCT ACAAAACAGA		
	~~~~~~~~~	<b>/~~~~</b>	MCEA		
4151			CATCACAGTC GTAGTGTCAG		

			MCEA		
4201		GCTGGGGCCA CGACCCCGGT			GTGCTGGTTG CACGACCAAC
	MCEA				
4251		GATATAGTTT CTATATCAAA			AGCCCGGGTT TCGGGCCCAA
		~~~	C3.	L Arm	
4301	TTTATAGCTA AAATATCGAT	ATTAGTCAAA TAATCAGTTT		TATTAGTATA ATAATCATAT	
•	~~~~~~~~~		C3L Arm		
4351	<u> </u>	ATATTCATTT TATAAGTAÄA			AGCTTTTATA TCGAAAATAT
•		(C3L Arm		
4401	AAACAATATA TTŢGTTATAT	ACTGAATAGT TGACTTATCA		CTAATAAGTT GATTATTCAA	
		(C3L Arm	,	
4451	GATACATATT CTATGTATAA	TATAGTATTT ATATCATAAA	TACTTTCTAC ATGAAAGATG		ATAATATAAT TATTATATTA
		(C3L Arm		
4501		TAATTTTTAA ATTAAAAATT	TACTATATAG ATGATATATC		AAATAAAATA TTTATTTTAT
•		(C3L Arm	,	1
4551	CCAGTGTAAT GGTCACATTA	ATAGTTATTA TATCAATAAT		CCACATCAAA GGTGTAGTTT	GATGAGTTAT CTACTCAATA
	2/		C3L Arm		
4601			CAACAGTAGT GTTGTCATCA	-	
		C	C3L Arm		
4651	TCGTATGGCG AGCATACCGC				
		~~~~~~~	C3L Arm	~~~	
4701	TAGGAAACGT ATCCTTTGCA				

	C3L Arm
4751	ATTATACCGT TTCTCAACTT GGGAATAGCC GATTTGCTGT TTGTGATAT TAATATGGCA AAGAGTTGAA CCCTTATCGG CTAAACGACA AACACTATA
	C3L Arm
4801	CATACCTTTA TACATTATAT ACATACTAAG TAATTTCCAT TGGCATTTT GTATGGAAAT ATGTAATATA TGTATGATTC ATTAAAGGTA ACCGTAAAA
	C3L Arm
4851	GTAAAGCACT TTGTAAAATT AGTTCTTTCT TTTTTACTTC TAACATGTT CATTTCGTGA AACATTTTAA TCAAGAAAGA AAAAATGAAG ATTGTACAA
	C3L Arm
4901	GCAAGTATAT TTTTAATAAC TGTAATAAGC GTATATAGAT ATGTAAAAA CGTTCATATA AAAATTATTG ACATTATTCG CATATATCTA TACATTTTT
	C3L Arm
4951	TACCCTTCCT GGATTTACCT ATAAATATGT TAACATTAGA AATATGTACATGGGAAGGA CCTAAATGGA TATTTATACA ATTGTAATCT TTATACATG
	C3L Arm
5001	TTACTATATT TTTCATATGG ATTATTTCTA TTATACTAGG GATTCCTGC AATGATATAA AAAGTATACC TAATAAAGAT AATATGATCC CTAAGGACG
	C3L Arm
5051	CTTTACTTTA GAAATACTAT CGTAACAAAA AATAACGACA CGCTGTGTA GAAATGAAAT CTTTATGATA GCATTGTTTT TTATTGCTGT GCGACACAT
	C3L Arm
5101	TAATCATTAT CATGATAATA GAGAAATTGC TGAATTGATT TACAAAGTT ATTAGTAATA GTACTATTAT CTCTTTAACG ACTTAACTAA ATGTTTCAA
	C3L Arm
5151	TTATCTGTAT CAGATTTATT TTAGGATACC TACTACCTAC GATAATTAT AATAGACATA GTCTAAATAA AATCCTATGG ATGATGGATG CTATTAATA
	. C3L Arm
5201	CTCGTATGCT ATACGTTACT GATCTACAGA ACTAACAATG CATGTCGAC GAGCATACGA TATGCAATGA CTAGATGTCT TGATTGTTAC GTACAGCTG
	C3L Arm
5251	CGGCCGCAA GCCGGCGTT